1

SEQUENCE LISTING

<110> SKERRA, ARNE
       FIEDLER, MARKUS

<120> SOLUBLE TRUNCATED POLYPEPTIDES OF THE NOGO-A PROTEIN

<130> 029029-0106

<140> 10/533,299
<141> 2005-04-29

<150> PCT/EP02/12210
<151> 2002-10-31

<160> 24

<170> PatentIn Ver. 3.3

<210> 1
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<212> PRT
<213> Rattus norvegicus

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Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
            35   40   45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
        50   55   60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
 65   70   75   80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
                85   90   95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
                100   105   110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
            115   120   125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
        130   135   140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145   150   155   160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
                165   170   175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
           180   185   190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
        195   200   205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
   210   215   220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225   230   235   240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
           245   250   255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
        260   265   270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
        275   280   285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
        290   295   300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305   310   315   320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
        325   330   335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
        340   345   350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
        355   360   365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
        370   375   380

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385   390   395   400

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
        405   410   415

Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
        420   425   430

Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
        435   440   445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
        450   455   460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465   470   475   480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
            485   490   495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
            500   505   510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
            515   520   525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
            530   535   540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545   550   555   560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
            565   570   575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
            580   585   590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
            595   600   605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
            610   615   620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625   630   635   640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
            645   650   655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
            660   665   670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
            675   680   685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
            690   695   700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705   710   715   720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
            725   730   735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
            740   745   750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
            755   760   765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
            770   775   780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
785   790   795   800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
            805   810   815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
        820   825   830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
        835   840   845

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
    850   855   860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865   870   875   880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
            885   890   895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
        900   905   910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
    915   920   925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
    930   935   940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945   950   955   960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val
            965   970   975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
        980   985   990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
    995   1000   1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
    1010   1015   1020

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu
1025   1030   1035   1040

Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu
            1045   1050   1055

Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser
            1060   1065   1070

Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp
    1075   1080   1085

Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala
    1090   1095   1100

Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe
1105   1110   1115   1120

Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr
         1125   1130   1135

Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln
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   1155   1160

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<211> 1192
<212> PRT
<213> Homo sapiens

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        20   25   30

Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
     35   40   45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
    50   55   60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65   70   75   80

Phe Gly Asn Glu Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
        85   90   95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
       100   105   110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
      115   120   125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
    130   135   140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145   150   155   160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
          165   170   175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
       180   185   190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Glu
      195   200   205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
      210   215   220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
225   230   235   240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Glu Asn Leu Ser
          245   250   255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
          260   265   270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
      275   280   285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
      290   295   300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
305   310   315   320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
          325   330   335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
          340   345   350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
      355   360   365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
      370   375   380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385   390   395   400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu
          405   410   415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
          420   425   430

Asn His Glu Lys Asn Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
      435   440   445

Ser Thr Pro Glu Gly Ile Lys Asp Arg Pro Gly Ala Tyr Ile Thr Cys
      450   455   460

Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe
465   470   475   480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
          485   490   495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr
          500   505   510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Glu Ser Glu Thr Asp
          515   520   525

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala
      530   535   540

Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
545   550   555   560

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
              565   570   575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
          580   585   590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
      595   600   605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
      610   615   620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625   630   635   640

Ala Ser Ser Val Gln Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
              645   650   655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
          660   665   670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
          675   680   685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
      690   695   700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Glu Phe Ser Asp Tyr Ser Glu
705   710   715   720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
              725   730   735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
              740   745   750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
          755   760   765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Gln
      770   775   780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785   790   795   800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
            805   810   815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Ile Gln Met
            820   825   830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
            835   840   845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
    850   855   860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865   870   875   880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
            885   890   895

Lys Ser Glu Ile Ala Gln Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
            900   905   910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
    ·   915   920   925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
    930   935   940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945   950   955   960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
            965   970   975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
            980   985   990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu
            995   1000   1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser
    1010   1015   1020

Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr
1025   1030   1035   1040

Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile
            1045   1050   1055

Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro
            1060   1065   1070

Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val
            1075   1080   1085

Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys
    1090   1095   1100

Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys
1105   1110   1115   1120

Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn
          1125   1130   1135

Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro
        1140   1145   1150

Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu
      1155   1160   1165

Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile
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Pro Gly Leu Lys Arg Lys Ala Glu
1185   1190

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<213> Artificial Sequence

<220>
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<210> 4
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<220>
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<210> 5
<211> 40
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
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<210> 6
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
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      primer

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ccc   63

<210> 7
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
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<223> a, c, g, t, unknown or other

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<222> (47)..(48)
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acagta                                                                66


<210> 10
<211> 75
<212> DNA
<213> Artificial Sequence

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      primer

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<222> (50)..(51)·
<223> a, c, g, t, unknown or other

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<221> modified_base
<222> (53)..(54)
<223> a, c, g, t, unknown or other

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acagtaatac gttgc                                                     75


<210> 11
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<213> Mus musculus

<400> 11
Glu Val Lys Leu His Glu Ser Gly Pro Gly Leu Val Arg Pro Gly Thr
  1               ·5                  10                  15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
               20                  25                  30

Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
           35                  40                  45

Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Asn Tyr Asn Glu Lys Phe
       50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                   85                  90                  95
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Ala Arg Phe Tyr Tyr Gly Ser Ser Tyr Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 12
<211> 107
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<213> Artificial Sequence

<220>
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      protein sequence

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Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
              20   '25   30

Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
          35   40   45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
      50   55   60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
 65   70   75   80

Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn Ile Asn Arg Val Pro Val
                  85   90   95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 13
<211> 2248
<212> DNA
<213> Artificial Sequence

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      nucleotide sequence

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<400> 13

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                         Met Lys Lys Thr Ala Ile Ala Ile Ala Val
                         -20                 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc tct ttt aaa gaa cat      99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe Lys Glu His
    -10                 -5              -1   1                   5

gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca att     147
Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile
                10                  15                  20

gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg gca aca     195
Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr
                25                  30                  35

aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat     243
Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr
            40                  45                  50

tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc     291
Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala
        55                  60                  65

ata tta gta gaa aac act aag gaa gaa gta att gtg agg agt aaa gac     339
Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp
70                  75                  80                  85

aaa gag gat tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca     387
Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser
                90                  95                  100

cct gtg ggt aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac     435
Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp
                105                 110                 115

att ttt aat gaa atg cag atg tca gta gta gca cct gtg agg gaa gag     483
Ile Phe Asn Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu
            120                 125                 130

tat gca gac ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act     531
Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr
    135                 140                 145

tat gag gga agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt     579
Tyr Glu Gly Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser
150                 155                 160                 165

aaa gtg gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt     627
Lys Val Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu
                170                 175                 180
```

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ggg aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc    675
Gly Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
            185             190             195

cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc    723
Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser
        200             205             210

ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta    771
Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu
        215             220             225

gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa    819
Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu
230             235             240             245

agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca aat    867
Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn
            250             255             260

cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt aca aca    915
Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr
            265             270             275

gat acc tta tca aag gtg act gag gca gca gtg tca aac atg cct gaa    963
Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu
        280             285             290

ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat   1011
Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn
        295             300             305

gaa gcc aca ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc   1059
Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val
310             315             320             325

caa aca tca gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt   1107
Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu
            330             335             340

tgc cca tca ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct   1155
Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro
            345             350             355

gat att gtt atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt   1203
Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly
            360             365             370

gct tct gta gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca   1251
Ala Ser Val Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro
            375             380             385

gtt agt tat gac agt ata aag ctt gag cct gaa aac ccc cca cca tat   1299
Val Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr
390             395             400             405
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gaa gaa gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga    1347
Glu Glu Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly
                410                 415                 420

ata aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct    1395
Ile Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
                425                 430                 435

cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc    1443
Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser
                440                 445                 450

act gag cca agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc    1491
Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe
        455                 460                 465

gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct    1539
Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro
470                 475                 480                 485

gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc    1587
Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val
                490                 495                 500

cca caa aca caa gag gag gct gtg atg ctc atg aag gag agt ctc act    1635
Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr
                505                 510                 515

gaa gtg tct gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc    1683
Glu Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala
                520                 525                 530

tca cct cag gag cta gga aag cca tat tta gag tct ttt cag ccc aat    1731
Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn
        535                 540                 545

tta cat agt aca aaa gat gct gca tct aat gac att cca aca ttg acc    1779
Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr
550                 555                 560                 565

aaa aag gag aaa att tct ttg caa atg gaa gag ttt aat act gca att    1827
Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile
                570                 575                 580

tat tca aat gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa    1875
Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu
                585                 590                 595

agt gaa aca ttt tca gat tca tct ccg att gag ata ata gat gaa ttt    1923
Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe
        600                 605                 610

ccc acg ttt gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag    1971
Pro Thr Phe Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu
        615                 620                 625
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tac act gat cta gaa gta tcc gac aaa agt gaa att gct aat atc caa      2019
Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln
630             635                 640                 645

agc ggg gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct      2067
Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser
                650                 655                 660

ttc aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc      2115
Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
                665                 670                 675

tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat      2163
Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
            680                 685                 690

gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa agc      2211
Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser
            695                 700                 705

gct tgg cgt cac ccg cag ttc ggt ggt taataagctt                       2248
Ala Trp Arg His Pro Gln Phe Gly Gly
710                 715
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<210> 14
<211> 2425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence

<220>
<221> CDS
<222> (22)..(2415)

<220>
<221> sig_peptide
<222> (22)..(84)

<220>
<221> mat_peptide
<222> (85)..(2415)

<400> 14

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tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg      51
                         Met Lys Lys Thr Ala Ile Ala Ile Ala Val
                         -20                 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gag acc ctt ttt gct      99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Glu Thr Leu Phe Ala
    -10                 -5              -1   1                   5

ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa aaa att      147
Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu Lys Ile
                10                  15                  20
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```
atg gat ttg atg gag cag cca ggt aac act gtt tcg tct ggt caa gag    195
Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly Gln Glu
            25                  30                  35

gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct tct cta    243
Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu
        40                  45                  50

tct cct ctc tca act gtt tct ttt aaa gaa cat gga tac ctt ggt aac    291
Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu Gly Asn
        55                  60                  65

tta tca gca gtg tca tcc tca gaa gga aca att gaa gaa act tta aat    339
Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr Leu Asn
 70                  75                  80                  85

gaa gct tct aaa gag ttg cca gag agg gca aca aat cca ttt gta aat    387
Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe Val Asn
                90                  95                  100

aga gat tta gca gaa ttt tca gaa tta gaa tat tca gaa atg gga tca    435
Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser
            105                 110                 115

tct ttt aaa ggc tcc cca aaa gga gag tca gcc ata tta gta gaa aac    483
Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn
        120                 125                 130

act aag gaa gaa gta att gtg agg agt aaa gac aaa gag gat tta gtt    531
Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val
        135                 140                 145

tgt agt gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa    579
Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu
150                 155                 160                 165

gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg    627
Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
                170                 175                 180

cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt aag    675
Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys
            185                 190                 195

cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt agg    723
Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg
        200                 205                 210

gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac aga aaa    771
Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys
        215                 220                 225

tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat agt gaa    819
Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu
230                 235                 240                 245
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ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct gtg aag    867
Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro Val Lys
                250                 255                 260

gac agc tcc aga gca tat att acc tgt gct tcc ttt acc tca gca acc    915
Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr
                265                 270                 275

gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat act tca    963
Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His Thr Ser
                280                 285                 290

gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc caa att   1011
Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala Gln Ile
                295                 300                 305

ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt gta gca   1059
Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu Val Ala
310                 315                 320                 325

gta cag gat tct gag gca gat tat gtt aca aca gat acc tta tca aag   1107
Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys
                330                 335                 340

gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg cca gat   1155
Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp
                345                 350                 355

tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca ggt aca   1203
Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr
                360                 365                 370

aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct   1251
Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala
                375                 380                 385

ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag   1299
Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu
390                 395                 400                 405

gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa   1347
Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
                410                 415                 420

gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg cag   1395
Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln
                425                 430                 435

ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat gac agt   1443
Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser
                440                 445                 450

ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc atg aat   1491
Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn
                455                 460                 465
```

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gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag cct gaa      1539
Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro Glu
470             475             480             485

agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata tcc att      1587
Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
            490             495             500

gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca agt cca      1635
Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro Ser Pro
            505             510             515

gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg gtg ccc      1683
Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser Val Pro
            520             525             530

gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa cca gtt      1731
Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu Pro Val
            535             540             545

gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca caa gag      1779
Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr Gln Glu
550             555             560             565

gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct gag aca      1827
Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser Glu Thr
            570             575             580

gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag gag cta      1875
Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu
            585             590             595

gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt aca aaa      1923
Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys
            600             605             610

gat gct gca tct aat gac att cca aca ttg acc aaa aag gag aaa att      1971
Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile
            615             620             625

tct ttg caa atg gaa gag ttt aat act gca att tat tca aat gat gac      2019
Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp
630             635             640             645

tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca      2067
Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser
            650             655             660

gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc agt      2115
Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser
            665             670             675

gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat cta gaa      2163
Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu
            680             685             690
```

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gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca gat tca    2211
Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser
    695             700             705

ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat ata tat    2259
Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile Tyr
710             715             720             725

cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat agg tcc    2307
Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn Arg Ser
            730             735             740

agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct ttg gaa    2355
Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala Leu Glu
            745             750             755

cct cag aca gaa atg ggc agc ata gtt aaa agc gct tgg cgt cac ccg    2403
Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Ala Trp Arg His Pro
        760             765             770

cag ttc ggt ggt taataagctt                                         2425
Gln Phe Gly Gly
    775


<210> 15
<211> 2278
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence

<220>
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<222> (22)..(2268)

<220>
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<222> (22)..(84)

<220>
<221> mat_peptide
<222> (85)..(2268)

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tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg    51
                        Met Lys Lys Thr Ala Ile Ala Ile Ala Val
                        -20             -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gct agc tgg agc cac    99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ala Ser Trp Ser His
    -10             -5              -1  1                       5

ccg cag ttc gaa aaa ggc gcc tct ttt aaa gaa cat gga tac ctt ggt   147
Pro Gln Phe Glu Lys Gly Ala Ser Phe Lys Glu His Gly Tyr Leu Gly
                10              15              20
```

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aac tta tca gca gtg tca tcc tca gaa gga aca att gaa gaa act tta    195
Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr Leu
            25                  30                  35

aat gaa gct tct aaa gag ttg cca gag agg gca aca aat cca ttt gta    243
Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe Val
        40                  45                  50

aat aga gat tta gca gaa ttt tca gaa tta gaa tat tca gaa atg gga    291
Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly
        55                  60                  65

tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc ata tta gta gaa    339
Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu
70                  75                  80                  85

aac act aag gaa gaa gta att gtg agg agt aaa gac aaa gag gat tta    387
Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu
                90                  95                  100

gtt tgt agt gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa    435
Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys
                105                 110                 115

gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa    483
Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu
        120                 125                 130

atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt    531
Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
        135                 140                 145

aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt    579
Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser
150                 155                 160                 165

agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac aga    627
Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg
                170                 175                 180

aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat agt    675
Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser
                185                 190                 195

gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct gtg    723
Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro Val
        200                 205                 210

aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc tca gca    771
Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala
        215                 220                 225

acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat act    819
Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His Thr
230                 235                 240                 245
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tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc caa      867
Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala Gln
            250                 255                 260

att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt gta      915
Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu Val
            265                 270                 275

gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta tca      963
Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu Ser
            280                 285                 290

aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg cca     1011
Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr Pro
            295                 300                 305

gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca ggt     1059
Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly
310                 315                 320                 325

aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca gaa     1107
Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu
            330                 335                 340

gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca ttt     1155
Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe
            345                 350                 355

gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt atg     1203
Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met
            360                 365                 370

gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg     1251
Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val
            375                 380                 385

cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat gac     1299
Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp
390                 395                 400                 405

agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc atg     1347
Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
            410                 415                 420

aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag cct     1395
Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro
            425                 430                 435

gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata tcc     1443
Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile Ser
            440                 445                 450

att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca agt     1491
Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro Ser
            455                 460                 465
```

```
cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg gtg       1539
Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser Val
470                 475             480                 485

ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa cca       1587
Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu Pro
                490             495                 500

gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca caa       1635
Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr Gln
            505             510                 515

gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct gag       1683
Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser Glu
        520                 525                 530

aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag gag       1731
Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu
        535             540                 545

cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt aca       1779
Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr
550                 555             560                 565

aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag aaa       1827
Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys
                570             575                 580

att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat gat       1875
Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp
                585             590                 595

gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt       1923
Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe
            600             605                 610

tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc       1971
Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val
        615             620                 625

agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat cta       2019
Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu
630                 635             640                 645

gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca gat       2067
Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp
                650             655                 660

tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat ata       2115
Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile
                665             670                 675

tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat agg       2163
Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn Arg
            680             685                 690
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tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct ttg   2211
Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala Leu
    695             700             705

gaa cct cag aca gaa atg ggc agc ata gtt aaa agc gct cac cat cac   2259
Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Ala His His His
710             715             720             725

cat cac cat taataagctt                                            2278
His His His
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<210> 16
<211> 798
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<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

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Thr Val Ala Gln Ala Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu
    -5              -1   1           5                       10

Pro Val Ile Pro Ser Ser Ala Glu Lys Ile Met Asp Leu Met Glu Gln
            15              20              25

Pro Gly Asn Thr Val Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu
            30              35              40

Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val
    45              50              55

Ser Phe Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser
60              65              70                          75

Ser Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
            80              85              90

Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe
            95              100             105

Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro
            110             115             120

Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile
            125             130             135

Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His
140             145             150             155

Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro
            160             165             170
```

Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser Val Val Ala
        175   180   185

Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala Trp
        190   195   200

Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp Val Leu Ala Ala Arg
        205   210   215

Ala Asn Val Glu Ser Lys Val Asp Arg Lys Cys Leu Glu Asp Ser Leu
220   225   230   235

Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala
            240   245   250

Ser Phe Pro Ser Thr Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr
            255   260   265

Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn
        270   275   280

Thr Phe Pro Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu
        285   290   295

Lys Lys Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser
300   305   310   315

Pro Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
            320   325   330

Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val
            335   340   345

Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys
            350   355   360

Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr
    365   370   375

Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr
380   385   390   395

Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro
            400   405   410

Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu
            415   420   425

Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro Ser Val Ser Pro Leu
        430   435   440

Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu
        445   450   455

Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn Val Ala Leu Lys Ala Leu
460   465   470   475

Gly Thr Lys Glu Gly Ile Lys Glu Pro Glu Ser Phe Asn Ala Ala Val
                480   485   490

Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys
            495   500   505

Glu Thr Lys Leu Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser
        510   515   520

Glu Ile Ala Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val
        525   530   535

Glu Asp Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp
540   545   550   555

Ser Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met
                560   565   570

Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu
            575   580   585

Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu
        590   595   600

Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp
    605   610   615

Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu
620   625   630   635

Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu
                640   645   650

Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu
            655   660   665

Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys Asp Asp Ser Pro
        670   675   680

Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser Glu
    685   690   695

Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu Leu
700   705   710   715

Pro Cys Asp Leu Ser Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His
                720   725   730

Val Ser Asp Glu Phe Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser
            735   740   745

Ile Ser Pro Ser Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly
        750   755   760

Ser Ile Val Lys Ser Ala Trp Arg His Pro Gln Phe Gly Gly
    765   770   775

<210> 17
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
       protein sequence

<400> 17
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
    -20   -15   -10

Thr Val Ala Gln Ala Ser Phe Lys Glu His Gly Tyr Leu Gly Asn Leu
 -5   -1   1   5   10

Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu
            15   20   25

Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg
        30   35   40

Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser
    45   50   55

Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr
 60   65   70   75

Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys
            80   85   90

Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
            95   100   105

Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln
        110   115   120

Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro
    125   130   135

Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp
140   145   150   155

Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys Cys
            160   165   170

Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu Gly
            175   180   185

Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro Val Lys Asp
        190   195   200

Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr Glu
    205   210   215

Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His Thr Ser Glu
220   225   230   235

```
Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala Gln Ile Ile
            240             245             250

Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu Val Ala Val
            255             260             265

Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val
            270             275             280

Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu
            285             290             295

Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys
300             305             310             315

Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile
            320             325             330

Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
            335             340             345

Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
            350             355             360

Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro
    365             370             375

Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile
380             385             390             395

Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn Val
            400             405             410

Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro Glu Ser
            415             420             425

Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala
            430             435             440

Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro Ser Pro Asp
    445             450             455

Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser Val Pro Glu
460             465             470             475

His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu Pro Val Asp
            480             485             490

Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr Gln Glu Glu
            495             500             505

Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val
            510             515             520

Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly
525             530             535
```

Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp
540   545   550   555

Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser
            560   565   570

Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu
        575   580   585

Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp
        590   595   600

Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala
    605   610   615

Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val
620   625   630   635

Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser Leu
            640   645   650

Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile Tyr Pro
        655   660   665

Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn Arg Ser Ser
        670   675   680

Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala Leu Glu Pro
    685   690   695

Gln Thr Glu Met Gly Ser Ile Val Lys Ser Ala Trp Arg His Pro Gln
700   705   710   715

Phe Gly Gly

<210> 18
<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     protein sequence

<400> 18
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
    -20   -15   -10

Thr Val Ala Gln Ala Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly
    -5   -1   1   5   10

Ala Ser Phe Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser
            15   20   25

Ser Ser Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu
        30   35   40

Leu Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
   45   50   55

Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser
60   65   70   75

Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val
          80   85   90

Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu
        95   100   105

His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val Ser
      110   115   120

Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser Val Val
    125   130   135

Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala
140   145   150   155

Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp Val Leu Ala Ala
        160   165   170

Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys Cys Leu Glu Asp Ser
        175   180   185

Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu Gly Arg Asn Glu Asp
      190   195   200

Ala Ser Phe Pro Ser Thr Pro Glu Pro Val Lys Asp Ser Ser Arg Ala
    205   210   215

Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala
220   225   230   235

Asn Thr Phe Pro Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp
        240   245   250

Glu Lys Lys Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr
        255   260   265

Ser Pro Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu
      270   275   280

Ala Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
    285   290   295

Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala
300   305   310   315

Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu
        320   325   330

Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu
      335   340   345

```
Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr
    350                 355             360

Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser
    365                 370             375

Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro Ser Val Ser Pro
380                 385                 390                 395

Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile Lys Leu Glu Pro
                400                 405                 410

Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn Val Ala Leu Lys Ala
            415                 420                 425

Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro Glu Ser Phe Asn Ala Ala
        430                 435                 440

Val Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile
    445                 450                 455

Lys Glu Thr Lys Leu Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr
460                 465                 470                 475

Ser Glu Ile Ala Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu
                480                 485                 490

Val Glu Asp Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp
            495                 500                 505

Asp Ser Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu
        510                 515                 520

Met Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys
    525                 530                 535

Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu
540                 545                 550                 555

Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser Asn
            560                 565                 570

Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln Met Glu
        575                 580                 585

Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys
        590                 595                 600

Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile
    605                 610                 615

Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys Asp Asp Ser
620                 625                 630                 635

Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser
            640                 645                 650
```

Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu
      655   660   665

Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val
      670   675   680

His Val Ser Asp Glu Phe Ser Glu Asn Arg Ser Ser Val Ser Lys Ala
      685   690   695

Ser Ile Ser Pro Ser Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met
700   705   710   715

Gly Ser Ile Val Lys Ser Ala His His His His His
          720   725

<210> 19
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     protein sequence

<400> 19
Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ala Ala Ser Val Gly
  1   5   10   15

Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
      20   25   30

Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
      35   40   45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
65   70   75   80

Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn Val Leu Ser Thr Pro Arg
        85   90   95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
        100   105

<210> 20
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     protein sequence

```
<400> 20
Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ala Ala Ser Val Gly
  1               5              10               15

Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Phe
             20              25              30

Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
         35              40              45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
     50              55              60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
 65              70              75              80

Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn Val Leu Ser Thr Pro Arg
             85              90              95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
             100             105
```

```
<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

<400> 21
Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ala Ala Ser Val Gly
  1               5              10               15

Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
             20              25              30

Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
         35              40              45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
     50              55              60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
 65              70              75              80

Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn Val Leu Arg Val Pro Cys
             85              90              95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
             100             105
```

<210> 22
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein sequence

<400> 22
Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ala Ala Ser Val Gly
1   5   10   15

Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
            20   25   30

Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
        35   40   45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
65   70   75   80

Asp Asp Val Ala Thr Tyr Tyr Cys Gln Asn Val Leu Arg Val Pro Val
                85   90   95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
5xHis tag

<400> 23
His His His His His
1   5

<210> 24
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 24
His His His His His His
1   5